

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:13:04 ; Search time 101.54 Seconds
(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089a-5

Perfect score: 286

Sequence: 1 RALCTICSDFFDHSRDVAAM.....IQSFETAPSRPCQCRIOVG 51

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	78.7	433	2 T30807	TRAF interacting p
2	114	39.9	310	2 C84701	hypothetical prote
3	113	39.5	158	2 T13738	hypothetical prote
4	112	39.2	325	2 F86321	FEA14.12 protein -
5	103	36.0	344	2 T05064	hypothetical prote
6	102	35.7	324	2 E84918	hypothetical prote
7	101	35.3	274	2 E48296	hypothetical prote
8	100	35.0	224	2 E86321	hypothetical prote
9	99	34.6	524	2 F96572	hypothetical prote
10	98	34.3	383	2 A86315	protein F12M16.10
11	95.5	33.4	506	2 F85016	F2H15.19 protein -
12	95	33.2	351	2 F96597	probable RING zinc
13	94	32.9	137	2 T46904	hypothetical prote
14	93	32.5	551	2 S6665	hypothetical prote
15	92.5	32.3	408	2 T25524	probable membrane
16	92.5	32.3	624	2 S28418	probable zinc-bind
17	92	32.2	489	2 T26069	hypothetical prote
18	91.5	32.0	441	2 F71425	hypothetical prote
19	90.5	31.6	206	2 C85067	hypothetical prote
20	90	31.5	190	2 T51859	hypothetical prote
21	89	31.1	367	2 H96764	protein RING zinc
22	89	31.1	292	2 T06684	hypothetical prote
23	89	31.1	425	2 T25457	hypothetical prote
24	88.5	30.9	405	2 A28009	43k postsynaptic m
25	87.5	30.6	157	2 T13027	RING-H2 finger pro
26	87.5	30.6	157	2 T51841	RING-H2 finger pro
27	87.5	30.6	194	2 C85130	hypothetical prote
28	87.5	30.6	203	2 T48129	hypothetical prote
29	87.5	30.6	425	2 A84849	probable RING zinc

30	86.5	30.2	477	2 JE0343	teif protein - rat
31	86.5	30.2	609	2 A43906	nuclear phosphopro
32	86	30.1	407	2 G96835	probable RING zinc
33	86	30.1	1238	2 T15919	hypothetical prote
34	85.5	29.9	227	2 T00428	hypothetical prote
35	85.5	29.9	1610	2 T11681	hypothetical prote
36	85	29.7	204	2 G84530	probable RING-H2 z
37	85	29.7	343	2 H96703	probable RING zinc
38	85	29.5	362	2 G84526	hypothetical prote
39	84.5	29.5	225	2 T04066	hypothetical prote
40	84.5	29.5	236	2 T04065	hypothetical prote
41	84.5	29.5	324	2 T08729	RING zinc finger p
42	84.5	29.5	412	2 S45064	nicotinic acetylch
43	84	29.4	513	2 TVH09F	ret finger protein
44	84	29.4	610	2 T22687	hypothetical prote
45	84	29.4	801	4 TVH09E	transforming prote

ALIGNMENTS

RESULT 1

T30807 TRAF interacting protein - Fugu rubripes

C:Species: Fugu rubripes

C>Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000

C:Accession: T30807

R:Cottage, A.J.; Clark, M.; Hawker, K.; Umranta, Y.; Wheller, D.; Bishop, M.; Elgar, F.E.B. Lett. 443, 370-374, 1999

A:Title: Three receptor genes for plasmalogen related growth factors in the genome of

A:Reference number: 220880; MUID:9148833

A:Accession: T30807

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-433 <COT>

A:Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1

A:Genetics:

A:Gene: TRIP

A:Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3

Query Match

78.7%; Score 225; DB 2; Length 433;

Best Local Similarity 76.0%; Pred. No. 8.7e-20;

Matches 38; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

OY 1 RALCTICSDFFDHSRDVAAMDCGHTFHLQCTIQSFETAPSRPCQCRIOV 50

Db 4 RALCTICSDFFDHSRDVAAMDCGHTFHLQCTIQSFETAPSRPCQCRIOV 53

RESULT 2

C84701 hypothetical protein At2g29840 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84701

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: C84701

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-310 <STO>

A:Cross-references: GB:AE002093; NID:g3582320; PIDN:AMC35217.1; GSPDB:GN00139

A:Gene: At2g29840

A:Map position: 2

Query Match 39.9%; Score 114; DB 2; Length 310;

Best Local Similarity 39.6%; Pred. No. 2e-06;
Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

OY 3 LCTICSDFFDHSRDVAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOV 50
Db 260 MCSICLDFDGRSIVLPCGHEFDECAIKWFT--NHDCPLCKRKL 305

RESULT 3

113738 hypothetical protein 22E5.12 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13738

R:Murphy, L.; Harris, D.; Barrell, B.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: 217668

A:Accession: T13738

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-158 <MUR>

A:Cross-references: EMBL:AL031765; NID:e1371523; PID:e1326038; PIDN:CABA1708.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000667

A:Introns: 41/2

A:Note: EG:22E5.12

C:Superfamily: RING finger homology

F:4-54/Domain: RING finger homology <RRN>

Query Match 39.5%; Score 113; DB 2; Length 158;
Best Local Similarity 48.9%; Pred. No. 1.5e-06;
Matches 23; Conservative 4; Mismatches 18; Indels 2; Gaps 1;

OY 3 LCTICSDFFDHSRDVAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOV 49
Db 7 ICTICSEKRTSDNIQAGSCGHAFFEDCL--DHMKRSQRTCPICRSQ 51

RESULT 4

F6A14.12 protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001

C:Accession: F86321

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: F86321

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-325 <STO>

A:Cross-references: GB:AE005172; NID:g6730707; PIDN:AAF27102.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 39.2%; Score 112; DB 2; Length 325;
Best Local Similarity 37.5%; Pred. No. 3.7e-06;
Matches 18; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

OY 3 LCTICSDFFDHSRDVAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOV 50
Db 276 VCTICLDFDGRSIVLPCGHEFDECAIKWFT--VRSHWCPLCKRKL 321

RESULT 5

T05064 hypothetical protein M3E9.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000

C:Accession: T05064

R:Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hohnsels, J.; Nemes, H.W.; Ma

submitted to the Protein Sequence Database, March 1999

A:Reference number: 215396

A:Accession: T05064

A:Molecule type: DNA

A:Residues: 1-344 <BEV>

A:Cross-references: EMBL:AL022223

A:Experimental source: cultivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A:Note: M3E9.170

C:Superfamily: RING finger homology

F:225-275/Domain: RING finger homology <RRN>

Query Match 36.0%; Score 103; DB 2; Length 344;
Best Local Similarity 38.3%; Pred. No. 4.8e-05;
Matches 18; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAAMDCGHTFHLOCLIOSFETAPSRTPCQCRIOV 50
Db 229 CSICLDFDGRSKAKKLCGHPHLCIOSAFNMKGAMCPCMR 273

RESULT 6

E84918 hypothetical protein At2g47700 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: E84918

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.W.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: E84918

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-324 <STO>

A:Cross-references: GB:AE002093; NID:g3738284; PIDN:AAC63626.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g47700

A:Map position: 2

Query Match 35.7%; Score 102; DB 2; Length 324;
Best Local Similarity 41.3%; Pred. No. 6e-05;
Matches 19; Conservative 6; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTIC--SDFDHSRDVAAMDCGHTFHLOCLIOSFETAPSRTPCQCR 47
Db 38 CSICLESVLDDGRSKAKKLCGHPHLCIOSAFNMKGAMCPCMR 83

RESULT 7

T48296 hypothetical protein Fg614.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000

C:Accession: T48296

R:Bevan, M.; Terryn, N.; Adiles, W.; Buysmaet, C.; Dasseville, R.; De Clerck, R.;

ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.

submitted to the Protein Sequence Database, April 2000

A:Reference number: 224491

A:Accession: T48296
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-274 <BEV>
A:Cross-references: EMBL:AL162973
A:Experimental source: cultivar Columbia; BAC clone F9G14
C:Genetics:
A:Map position: 5
A:Note: F9G14.60
C:Superfamily: RING finger homology
F:201-251/Domain: RING finger homology <RRN>

Query Match 35.3%; Score 101; DB 2; Length 274;
Best Local Similarity 38.3%; Pred. No. 6.8e-05;
Matches 18; Conservative 6; Mismatches 21; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAAAMDCGTHFLQCLIOSEFTAPSTPCQCRIOV 50
Db 205 CVICKEKSEGRDYCEMPCQHFFHMKCILPWL--SKNKCPCFCHPQL 249

RESULT 8
E86321
hypothetical protein F6A14.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: E86321
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E86321
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <STO>
A:Cross-references: GB:AE005172; NID:96730708; PIDN:AAF27103.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 35.0%; Score 100; DB 2; Length 224;
Best Local Similarity 38.3%; Pred. No. 7.5e-05;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAAAMDCGTHFLQCLIOSEFTAPSTPCQCRIOV 50
Db 175 CTICLEEFNDGTYKWTLPCHGEHFEDECVLTFEFT--NHDCPLCPKRL 219

RESULT 9
F96572
protein F12M16.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96572
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719
A:Accession: F96572
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-524 <STO>
A:Cross-references: GB:AE005173; NID:97769853; PIDN:AAF69531.1; GSPDB:GN00141
C:Genetics:
A:Gene: F12M16.10
A:Map position: 1

Query Match 34.6%; Score 99; DB 2; Length 524;
Best Local Similarity 36.4%; Pred. No. 0.00021;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAAAMDCGTHFLQCLIOSEFTAPSTPCQCR 47
Db 472 CTICQSEFKNEKATLTDGHEHAECLKWL--IVKNVCPICK 513

RESULT 10
A86315
F2H15.19 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: A86315
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maltli, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A86315
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: GB:AE005172; NID:99665074; PIDN:AAF97276.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 34.3%; Score 98; DB 2; Length 383;
Best Local Similarity 34.1%; Pred. No. 0.00021;
Matches 15; Conservative 11; Mismatches 16; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAAAMDCGTHFLQCLIOSEFTAPSTPCQCR 47
Db 335 CSTICDEYEREDEVGELNCGSFHVHCYKWL--SRKNACPVCK 376

RESULT 11
F85016
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: F85016
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: F85016
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <STO>
A:Cross-references: GB:NC_001268; NID:97267624; PIDN:CAB80936.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g01270
A:Map position: 4

RESULT 16
S28418
probable zinc-binding protein - Iberian ribbed newt
C:Species: Pleurodeles waltlil (Iberian ribbed newt)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jan-2000
C:Accession: S28418; S29476
R:Belini, M.; Lacroix, J.C.; Gall, J.G.
EMBO J. 12, 107-114, 1993
A:Title: A putative zinc-binding protein on lampbrush chromosome loops.
A:Reference number: S28418; MUID:93154311
A:Accession: S28418
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <BEL>
A:Cross-references: EMBL:L04190
R:Belini, M.; Lacroix, J.C.; Gall, J.G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29476
A:Accession: S29476
A:Molecule type: mRNA
A:Residues: 1-263, 'LK', 266-624 <BE2>
A:Cross-references: EMBL:L04190; NID:g213867; PID:g213868
C:Comment: This DNA-binding phosphoprotein is enriched in nuclei of adult brain cells and
C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology
C:Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F:158-207/Domain: RING finger homology <RNG>

Query Match 32.3%; Score 92.5; DB 2; Length 624;
Best Local Similarity 31.8%; Pred. No. 0.0015;
Matches 14; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSRTPCQRIQV 47
Db 162 CPICRSIF--KEPVILCEGHNFCKHCDKSWESASAFSCECK 202

RESULT 17
T26069
hypothetical protein W02A11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T26069
R:White, S.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20147
A:Accession: T26069
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-489 <WIL>
A:Cross-references: EMBL:Z82062; PIDN:CAB04890.1; GSPDB:GN00019; CESP:W02A11.3
A:Experimental source: clone W02A11
C:Genetics:
A:Gene: CESP:W02A11.3
A:Map position: 1
A:Introns: 58/3; 129/3; 361/3; 444/3
C:Superfamily: RING finger homology
F:429-479/Domain: RING finger homology <RRN>

Query Match 32.2%; Score 92; DB 2; Length 489;
Best Local Similarity 27.7%; Pred. No. 0.0014;
Matches 13; Conservative 12; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLOCLIOSEFTAPSRTPCQRIQV 50
Db 433 CTVCISFDEGDSIOKRCNHVFHECIYKWLDI--NKRCPMCREEI 477

RESULT 18
F71425
hypothetical protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000
C:Accession: F71425
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; G
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B
Nature 391, 485-488, 1998
A:Authors: Mueller-Auer, S.; Silvea, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen
erhoff, A.; Moors, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t
A:Reference number: A71400; MUID:98121113
A:Accession: F71425
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-441 <BEV>
A:Cross-references: GB:297340; NID:g2244950; PID:e326963; PID:g2244955
C:Genetics:
A:Map position: 4COP9-4G3845
C:Superfamily: RING finger homology
F:278-329/Domain: RING finger homology <RRN>

Query Match 32.0%; Score 91.5; DB 2; Length 441;
Best Local Similarity 37.5%; Pred. No. 0.0015;
Matches 18; Conservative 9; Mismatches 18; Indels 3; Gaps 2;

OY 4 CTIC-SDFDHSRDVAMDCGHTFHLOCLIOSEFTAPSRTPCQRIQV 50
Db 282 CVCILSEKDNESGRVMPCKRFTFVHCIDMWFHSHS--CPICRSQI 327

RESULT 19
C85067
hypothetical protein AT4g05350 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C:Accession: C85067
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488
A:Accession: C85067
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STO>
A:Cross-references: GB:NC_001268; NID:g7267295; PIDN:CAB81077.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g05350
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING

Query Match 31.6%; Score 90.5; DB 2; Length 206;
Best Local Similarity 36.0%; Pred. No. 0.001;
Matches 18; Conservative 7; Mismatches 20; Indels 5; Gaps 2;

OY 4 CTICSDFF---DHSRDVAMDCGHTFHLOCLIOSEFTAPSRTPCQRIQV 50
Db 157 CSICLESIVSGPKPRDVRMTCSHFVHNGCLEWLKLR--KNTCPICRREI 204

RESULT 20
T51859
RING-H2 finger protein RHGla [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51859
R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 283-7, 1998
A:Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the
A:Reference number: Z13771; MUID:98452956
A:Accession: T51859

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-190 <JEN>
A:Cross-references: EMBL:AF079183; PIDN:AAC69857.1

Query Match 31.5%; Score 90; DB 2; Length 190;
Best Local Similarity 29.5%; Pred. No. 0.0011;
Matches 13; Conservative 10; Mismatches 19; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHQCLIOSEFTAPSTPCQCR 47
Db 136 CCVCEYTEGEDMCTLECGHFHSQCIEMWLK--QKNLCPICK 177

RESULT 21

H96764
Protein RING zinc finger protein F25P22.18 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96764
R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719

A:Accession: H96764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-367 <STO>
A:Cross-references: GB:AE005173; NID:96692739; PIDN:AAF24845.1; GSPDB:GN00141
C:Genetics:
A:Gene: F25P22.18
A:Map position: 1

Query Match 31.5%; Score 90; DB 2; Length 367;
Best Local Similarity 34.1%; Pred. No. 0.0019;
Matches 15; Conservative 8; Mismatches 19; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHQCLIOSEFTAPSTPCQCR 47
Db 319 CIIODEYEAREDEVELGELRGHRFHIDCVNWL--VRKNSCPVCK 360

RESULT 22

T06684
hypothetical protein T17F15.140 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-Sep-2000
C:Accession: T06684
R:Queller, F.; Choinsne, N.; Robert, C.; Brotlier, P.; Wincker, P.; Catcolico, L.; Artig
submitted to the Protein Sequence Database, April 1999

A:Reference number: Z15793
A:Accession: T06684
A:Molecule type: DNA
A:Residues: 1-292 <OUE>
A:Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.140
A:Experimental source: cultivar Columbia; BAC clone T17F15
C:Genetics:
A:Gene: ATSP:T17F15.140
A:Map position: 3
A:Introns: 37/3; 68/3; 90/3; 143/3; 181/3
C:Superfamily: RING zinc finger homology
F:105-215/Domain: RING zinc finger homology <RRN>

Query Match 31.1%; Score 89; DB 2; Length 292;
Best Local Similarity 34.0%; Pred. No. 0.0021;
Matches 16; Conservative 8; Mismatches 21; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHQCLIOSEFTAPSTPCQCR 50
Db 169 CLICIEFHIGHEVRLPCAHNFHECIDQWLR--NVKCPRCRSV 213

RESULT 23

T23457
hypothetical protein B0432.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T23457
R:Henkhaus, J.; Wohldmann, P.
submitted to the EMBL data library, December 1996
A:Description: The sequence of C. elegans cosmid B0432.
A:Reference number: 220038
A:Accession: T23457

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-425 <HEN>
A:Cross-references: EMBL:U80836; PIDN:AB37893.1; GSPDB:GN00020; CESP:B0432.9
A:Experimental source: strain Bristol N2; clone B0432
C:Genetics:
A:Gene: CESP:B0432.9
A:Map position: 2
A:Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2
C:Superfamily: RING zinc finger homology
F:188-238/Domain: RING zinc finger homology <RRN>

Query Match 31.1%; Score 89; DB 2; Length 425;
Best Local Similarity 36.4%; Pred. No. 0.0029;
Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

Y 4 CTICSDFFDHSRDVAMDCGHTFHQCLIOSEFTAPSTPCQCR 47
Db 192 CIICFEDIKQNDKISAIYCGIHHGCLISOWIAT--KRQPCSR 233

RESULT 24

A28009
43K postsynaptic membrane protein - Pacific electric ray

C:Species: Torpedo californica (Pacific electric ray)
C:Date: 19-May-1989 #sequence_revision 12-Mar-1993 #text_change 01-Dec-2000
C:Accession: A28009; B60088; I50550; I50551
R:Garr, C.; McCourt, D.; Cohen, J.B.
Biochemistry 26, 7090-7102, 1987
A:Title: The 43-kilodalton protein of Torpedo nicotinic postsynaptic membranes: purif
A:Reference number: A28009; MUID:88107644

A:Accession: A28009
A:Molecule type: protein
A:Residues: 1-386; 'D', 388-403, 'T', 405 <CA2>
R:Baldwin, T.J.; Theriot, J.A.; Yoshinara, C.M.; Burden, S.J.
Development 104, 557-564, 1988
A:Title: Regulation of transcript encoding the 43K subunit protein during develop
A:Reference number: A60088; MUID:90032364

A:Accession: B60088
A:Status: nucleic acid sequence not shown: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 364-405 <BAL>

R:Fall, D.E.; Mudd, J.; Shah, V.; Garr, C.; Cohen, J.B.; Merlie, J.P.
Proc. Natl. Acad. Sci. U.S.A. 84, 6302-6306, 1987

A:Title: cDNAs for the postsynaptic 43-kDa protein of Torpedo electric organ encode t
A:Reference number: I50550; MUID:87317641

A:Accession: I50550
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'MGDOQTK', 1-354, 'Y', 356-382 <FRA>
A:Cross-references: GB:J02952; NID:g213240; PIDN:AAA49282.1; PID:g213241
A:Accession: I50551

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 364-405 <FR2>
A:Cross-references: GB:002953; NID:g213242; PIND:AAA49283.1; PID:g213243
A:Comment: This protein is present in the postsynaptic apparatus at equimolar amounts w
K:Keywords: alternative splicing; cytoskeleton; membrane protein; phosphoprotein

Query Match	30.9%	Score	88.5	~DB	2	Length	405
Best Local Similarity	35.6%	Pred. No.	0.0032				
Matches	16	Conservative	9	Mismatches	15	Indels	5
						Gaps	2

QY 4 CTICSDFF-DHSRDVAMDCGHTFHLQCLIQSFETAPSRTPCQR 47
 | : | : | : | : | : | : | : | : | : | : | :
Db 356 CGLGESIGDQNSQLDALPCSHLFLHKL---QTNGNRGPCPNCK 396

RESULT	25
T13027	
RING-H2 finger protein RHA1b - Arabidopsis thaliana	
N:Alternate names: protein ER131 150	

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 02-Sep-2000
C/Accession: T113027
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dijkse, W.; Stiekema, W.; Bancroft, I.; Meunier, J.-F.
Submitted to the Protein Sequence Database, July 1999
A/Reference number: Z17587

A:Residues:1-157 <BE>
A:Cross-references:EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.150
A:Experimental source: cultivar Columbia; BAC clone F8L21
C:Genetics:
A:Gene: ATSP:F8L21.150

C;Superfamily: RING finger homology
F;81-134/Domain: RING finger homology <RRN>

Query Match	30.6%	Score 87.5	DB 2	Length 157
Best Local Similarity	40.0%	Pred. No.	0.0018	
Matches 18	Conservative 4	Mismatches 22	Indels 1	Gaps 1

QY 4 CTTC-SDFFDHSRDVAAMDCGHTFHLQCLIQSFETAPSRTPQGR 47
 ||:| ||| : ||| |:| : ||| ||
 Db 85 CTVCLSDFVSDDKIRQLPKCGHVFHHRCLDRWIVDCKNTCPICR 129

RESULT 26
T51841

RING-H2 finger protein RHA1b [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: T51841
R:Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
EMBL: At1g 283-7 1998

A:Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mouse
A:Decid: 19980307 1350
A:Reference number: 213771; MUID:98452956
A:Accession: J51841
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-157 <JRN>
A:Cross-references: EMBL:AF078821; PIRN:AA06670.1
A:Experimental source: cultivated Columbia

Query Match	30.68;	Score 87.5;	DB 2;	Length 157;
Best Local Similarly	40.08;	Pred. No. 0.0018;		
Matches 18; Conservative	4;	Mismatches 22;	Indels 1;	Gaps 1

```

QY      4 CTIC-SDFFEDHSRDVAAMDCGHTFHLQCLIOSFETAPSRTCPOCR 47
      ||:| ||| : ||| ||: ||| : ||| ||
Db      85 CTVCLSDFVSDDKIRQLPKCGHVFHHRCLDRWIVDCKKITCPICR 129

```

RESULT 27
C85130
hypothetical protein AT4g12190 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
Accession: C85130

R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2000.
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488

A:Accession: C85130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <STO>
A:Cross-references: GB:NC_001268; NID:97267920; PIDN:CB78262.1; GSPDB:GN00140

C:genetics: 1
A:Gene: AT4g12190
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J3.210; RING

Query Match	30.68	Score 87.5	DB 2	Length 194
Best Local Similarity	34.08	Pred. No. 0.0022		
Matches 17	Conservative	8	Mismatches 20	Indels 5
				Gaps 2

```

Oy      4  CTCISDF---DHSRDVAAMDCGHTFHLQCLIQSFETARSPTCPQCRIGV 50
          |:::  |::  |::  |::  |::  |::  |::  |::  |::  |::
Db      145 CSICLESIVSGPKPRDITRMTCSHVFHNGCLLEWLR--KNTCPICRTEL 192

```

hypothetical protein TMC9.30 - *Arabidopsis thaliana*
Species: *Arabidopsis thaliana* (mouse-ear cress)
T48129 RESULT 28

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: T48129
R;By: van Staveren, M.; Dirse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, June 1999

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A:Reference number: Z2485
A:Accession: T48129
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <BEV>

```

A; Cross-References: EMBL:AF080518
A; Experimental source: cultivar Columbia, BAC clone T4C9
C; Genetics:
A; Map position: 4
A; Introns: 9/3
A; Note: T4C9 30

Query Match 30.6% Score 87.5 DB 2: length 203:
C:Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING
F;150-203/Domain: RING finger homology <RNR>

Best Local Similarity 34.0%; Pred. NO. 0.0023;
Matches 17; Conservative 8; Mismatches 20; Indels 5; Gaps 2

QY 4 CTICSDFF---DHSRDVAAMDCGHTFHIOCLIQSPETAPSRPCQRIQV 50
||| : ||| | | | | | | | | | | | | | | | |
Gb 154 CIGLESLVSGPKPRDITRMTCSHVENHGKLEWLR--KNCPCLCRTEL 201

RESULT 29
A84849
probable RING zinc finger protein [imported] - Arabidopsis thaliana

C/Species: *Arbidiopsis thaliana* (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: A84849
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
B.; Koo, H.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
A.; Koo, H.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter


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RESULT      34
T000428
hypothetical protein Atg947560 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T30B22.14
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T000428; G84916
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
submitted to the EMBL Data Library, October 1998
A:Description: Arabidopsis thaliana Chromosome II BAC T30B22 genomic sequence.
A:Reference number: Z14149
A:Accession: T000428
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-227 <ROUT>
A:Cross-references: EMBL:AC002535; NID:g2529657; PID:g2529671
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;
M.: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Unayama, L.; Tallon, L.
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84916
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <STO>
A:Cross-references: GB:AE002093; NID:g2529671; PID:AAC62854.1; GSPDB:GN00139
C:Genetics:
A:Gene: T30B22.14; ATg947560
A:Map position: 2
C:Superfamily: Arabidopsis hypothetical protein F1913.22; RING finger homology
F:104-135/Domain: RING finger homology <RRN>

Query Match          29.9%; Score 85.5; DB 2; Length 227;
Best Local Similarity 35.4%; Pred. No. 0.0044;
Matches 17; Conservative 8; Mismatches 20; Indels 3; Gaps 2;

QY      4 CTTC-SDFPDHSRDVAAADCCHTFHACLIOSEFTAPSRGPCORIQV 50
       ||::||:         ||::||:   |   |   ||| || |
Db     108 CSVCLSEFEDEDEGRLLPKCGSHFVDCIDTWFRS-RSTGCLCAPV 153

RESULT      35
T11681
hypothetical protein SPBC21D10.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T11681
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z17313
A:Accession: T11681
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1610 <SEE>
A:Cross-references: EMBL:AL031536; NID:e1319499; PID:e1319508
A:Experimental source: strain 972h(-)
C:Genetics:
A:Map position: IIR
A:Introns: 10/2
A>Note: SPBC21D10.09c
C:Superfamily: RING finger homology
F:1554-1609/Domain: RING finger homology <RRN>

Query Match          29.9%; Score 85.5; DB 2; Length 1610;
Best Local Similarity 36.2%; Pred. No. 0.026;
Matches 17; Conservative 5; Mismatches 22; Indels 3; Gaps 1;

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Ox      4      CTICSDFFDHSRDVAAMDCGHTFHLOCLIQSFETAPSPQCQCRQV 47
          | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1558  CALCYSLVSLVERTLPNKRRCGTCRKRHFHASCILYKWFKSNSSRCPCLR 1604

RESULT# 36

Probable RING-H2 zinc finger protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence.revision 02-Feb-2001 #text.change 02-Feb-2001
C:Accession: G84530
R:Rltb, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffett, K.S.; Crokin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
Euss, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1:204 <STO>
A:Cross-references: GB:AE002093; NID:g4335724; PIDN:AAD17402.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g15580
A:Map position: 2

Query Match      29.7%; Score 85; DB 2; Length 204;
Best Local Similarity 34.0%; Pred. No. 0.0046;
Matches 16; Conservative 6; Mismatches 23; Indels 2; Gaps 1;

Ox      4      CTICSDFFDHSRDVAAMDCGHTFHLOCLIQSFETAPSPQCQCRQV 50
          | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      158  CALCDRFFKKGETLVHLPCKAHRFHSICLLPMIDT--NVCPCYCRDI 202

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RESULT      37
H96703
probable RING zinc finger protein T2K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96703
R:Phlogis, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alon
Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, T.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallio
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallio
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: H96703
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-43 <STO>
A:Cross-references: GB:AEO05173; NID:96553889; PIDN:AAF16555.1; GSPDB:GN00141
C:Genetics:
A:Gene: T2K23.8
A:Map position: 1

Query Match          29.7%; Score 85; DB 2; Length 343;
Best Local Similarity 25.5%; Pred No. 0.0074;
Matches 12; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY      4 CTCTGDFDHSRDVAMDCGHTFHLQCLIQSFETASRTCPQCRIQV 50
       111:::| | | | | | | | | | | | | | | | | | | |
Db      292 CCICLSYEDGAELVSLPCNNHHFSTCIATKLKM--NATCPICKRNI 336

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